RAW SEQUENCE LISTING

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Application Serial Number: _____ 10/560,961 _____

Source: _____ JFWP _____

Date Processed by STIC: _____ 12/30/2005 _____

ENTERED

RAW SEQUENCE LISTING   DATE: 12/30/2005
PATENT APPLICATION: **US/10/560,961**   TIME: 09:43:13

Input Set : **A:\15450PCT00.ST25.txt**
Output Set: **N:\CRF4\12302005\J560961.raw**

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 3  <110> APPLICANT: Pharmexa A/S
 5  <120> TITLE OF INVENTION: PURIFICATION OF HER-2 VARIANTS
 7  <130> FILE REFERENCE: P1020DK00
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C--> `9  <140> CURRENT APPLICATION NUMBER: US/10/560,961`
C--> `9  <141> CURRENT FILING DATE: 2005-12-14`
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 9  <160> NUMBER OF SEQ ID NOS: 2
11  <170> SOFTWARE: PatentIn version 3.2
13  <210> SEQ ID NO: 1
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15  <212> TYPE: DNA
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25  <223> OTHER INFORMATION: SV40 late polyadenylation site
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64 <223> OTHER INFORMATION: Dipeptidase stop sequence
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69 <223> OTHER INFORMATION: Gene coding for the hHER2MA5-5DUH protein
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74 <223> OTHER INFORMATION: Diphtheria toxoid P2 epitope
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152 atccgtaaga tgctttttctg tgactggtga gtactcaacc aagtcattct gagaatagtg  2160
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168 aaccattatt atcatgacat taacctataa aaataggcgt atcacgaggc cctttcgttc  2640
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198 gatcggggta ccaaagtcac c atg aag ttg tgc atc ttg ctg gcc gtc gtg  3531
199                          Met Lys Leu Cys Ile Leu Leu Ala Val Val
200                                          -15                -10
202 gcc ttc gtg ggc ctg tcg ctg ggc atg aag cac caa cac caa cat caa  3579
203 Ala Phe Val Gly Leu Ser Leu Gly Met Lys His Gln His Gln His Gln
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206 cat caa cat caa cat caa gcc ccc tcc acc caa gtg tgt acc ggc aca  3627
207 His Gln His Gln His Gln Ala Pro Ser Thr Gln Val Cys Thr Gly Thr
208     10                    15                20
210 gac atg aag ctg cgg ctc cct gcc agt ccc gag acc cac ctg gac atg  3675
211 Asp Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
212 25                    30                35                40
214 ctc cgc cac ctc tac cag ggc tgc cag gtg gtg cag gga aac ctg gaa  3723
215 Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu
216             45                50                55
218 ctc acc tac ctg ccc acc aat gcc agc tta agt ttc ctg cag gat atc  3771
219 Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile
220             60                65                70
222 cag gag gtg cag ggc tac gtg ctc atc gct cac aac caa gtg agg cag  3819
223 Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln
224         75                80                85
226 gtc cca ctg cag agg ctg cgg att gtg cga ggc acc cag ctc ttt gag  3867
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227 Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu
228     90                95                100
230 gac aac tat gcc ctg gcc gtg cta gac aat gga gac ccg ctg aac aat   3915
231 Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn
232 105               110               115                  120
234 acc acc cct gtc aca ggg gcc tcc cca gga ggc ctg cgg gag ctg cag   3963
235 Thr Thr Pro Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln
236               125               130               135
238 ctt cga agc ctc aca gag atc ttg aaa gga ggg gtc ttg atc cag cgg   4011
239 Leu Arg Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg
240               140               145               150
242 aac ccc cag ctc tgc tac cag gac acg att ttg tgg aag gac atc ttc   4059
243 Asn Pro Gln Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe
244       155               160               165
246 cac aag aac aac cag ctg gct ctc aca ctg ata gac acc aac cgc tct   4107
247 His Lys Asn Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser
248     170               175               180
250 cgg gcc tgc cac ccc tgt tct ccg atg tgt aag ggc tcc cgc tgc tgg   4155
251 Arg Ala Cys His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp
252 185               190               195                  200
254 gga gag agt tct gag gat tgt cag agc ctg acg cgc act gtc tgt gcc   4203
255 Gly Glu Ser Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala
256               205               210               215
258 ggt ggc tgt gcc cgc tgc aag ggg cca ctg ccc act gac tgc tgc cat   4251
259 Gly Gly Cys Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His
260               220               225               230
262 gag cag tgt gct gcc ggc tgc acg ggc ccc aag cac tct gac tgc ctg   4299
263 Glu Gln Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu
264       235               240               245
266 gcc tgc ctc cac ttc aac cac agt ggc atc tgt gag ctg cac tgc cca   4347
267 Ala Cys Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro
268     250               255               260
270 gcc ctg gtc cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc   4395
271 Ala Leu Val Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr
272 265               270               275                  280
274 gag ctg cgg tat aca ttc ggc gcc agc tgt gtg act gcc tgt ccc tac   4443
275 Glu Leu Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr
276               285               290               295
278 aac tac ctt tct acg gac gtg gga tcc tgc acc ctc gtc tgc ccc ctg   4491
279 Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu
280               300               305               310
282 cac aac caa gag gtg aca gca gag gat gga aca cag cgg tgt gag aag   4539
283 His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys
284               315               320               325
286 tgc agc aag ccc tgt gcc cga gtg tgc tat ggt ctg ggc atg gag cac   4587
287 Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His
288     330               335               340
290 ttg cga gag gtg agg gca gtt acc agt gcc aat atc cag gag ttt gct   4635
291 Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala
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295 Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe
296                   365                   370                   375
298 gat ggg gac cca gcc tcc aac act gcc ccg ctc cag cca gag cag ctc        4731
299 Asp Gly Asp Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu
300                   380                   385                   390
302 caa gtg ttt gag act ctg gaa gag atc aca ggt tac cta tac atc tca        4779
303 Gln Val Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser
304             395                   400                   405
306 gca tgg ccg gac agc ctg cct gac ctc agc gtc ttc cag aac ctg caa        4827
307 Ala Trp Pro Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln
308       410                   415                   420
310 gta atc cgg gga cga att ctg cac aat ggc gcc tac tcg ctg acc ctg        4875
311 Val Ile Arg Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu
312 425                   430                   435                   440
314 caa ggg ctg ggc atc agc tgg ctg ggg ctg cgc tca ctg agg gaa ctg        4923
315 Gln Gly Leu Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu
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318 ggc agt gga ctg gcc ctc atc cac cat aac acc cac ctc tgc ttc gtg        4971
319 Gly Ser Gly Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val
320                   460                   465                   470
322 cac acg gtg ccc tgg gac cag ctc ttt cgg aac ccg cac caa gct ctg        5019
323 His Thr Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu
324             475                   480                   485
326 ctc cac act gcc aac cgg cca gag gac gag tgt gtg ggc gag ggc ctg        5067
327 Leu His Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu
328       490                   495                   500
330 gcc tgc cac cag ctg tgc gcc cga ggg cac tgc tgg ggt cca ggg ccc        5115
331 Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro
332 505                   510                   515                   520
334 acc cag tgt gtc aac tgc agc cag ttc ctt cgg ggc cag gag tgc gtg        5163
335 Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val
336                   525                   530                   535
338 gag gaa tgc cga gta ctg cag ggg ctc ccc agg gag tat gtg aat gcc        5211
339 Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala
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344       555                   560                   565
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347 Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His
348       570                   575                   580
350 tat aag gac cct ccc ttc tgc gtg gcc cgc tgc ccc agc ggt gtg aaa        5355
351 Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys
352 585                   590                   595                   600
354 cct gac ctc tcc tac atg ccc atc tgg aag ttt cca gat gag gag ggc        5403
355 Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly
356                   605                   610                   615
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date